SEQUENCE LISTING

(1) GENERAL INFORMATION:

  (i) APPLICANT: Gregory Plowman
                                       Douglas Clary

 (ii) TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
                                         Alk-7 RELATED DISORDERS

(iii) NUMBER OF SEQUENCES: 15

 (iv) CORRESPONDENCE ADDRESS:

     (A)   ADDRESSEE: Lyon & Lyon
     (B)   STREET: 633 West Fifth Street
                              Suite 4700
     (C)   CITY: Los Angeles
     (D)   STATE: California
     (E)   COUNTRY: U.S.A.
     (F)   ZIP: 90071-2066

  (v) COMPUTER READABLE FORM:

     (A)   MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                              storage
     (B)   COMPUTER: IBM Compatible
     (C)   OPERATING SYSTEM: IBM P.C. DOS 5.0
     (D)   SOFTWARE: FastSEQ for Windows 2.0

 (vi) CURRENT APPLICATION DATA:

     (A)   APPLICATION NUMBER: To be assigned
     (B)   FILING DATE: Filed herewith
     (C)   CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

     (A)   APPLICATION NUMBER: 60/044,428
     (B)   FILING DATE: April 28, 1997

(viii) ATTORNEY/AGENT INFORMATION:

     (A)   NAME: Warburg, Richard J.
     (B)   REGISTRATION NUMBER: 32,327
     (C)   REFERENCE/DOCKET NUMBER: 234/118

 (ix) TELECOMMUNICATION INFORMATION:

     (A)   TELEPHONE: (213) 489-1600
     (B)   TELEFAX: (213) 955-0440
     (C)   TELEX: 67-3510

(2)   INFORMATION FOR SEQ ID NO: 1:

    (i)   SEQUENCE CHARACTERISTICS:

        (A)   LENGTH: 1793 base pairs
        (B)   TYPE: nucleic acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY: linear

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 1:

```
CGGCCACACT GACTAGAGCC AACCGCGCAC TTCAAAAGGG TGTCGGTGCC GCGCTCCCCT    60
CCCGCGGCCC GGGAACTTCA AAGCGGGCCG TGCTGCCCCG GCTGCCTCGC TCTGCTCTGG   120
GGCCTCGCAG CCCCGGCGCG GCCGCCTGGT GGCGATGACC CGGGCGCTCT GCTCAGCGCT   180
CCGCCAGGCT CTCCTGCTGC TCGCAGCGGC CGCCGAGCTC TCGCCAGGAC TGAAGTGTGT   240
ATGTCTTTTG TGTGATTCTT CAAACTTTAC CTGCCAAACA GAAGGAGCAT GTTGGGCATC   300
AGTCATGCTA ACCAATGGAA AAGAGCAGGT GATCAAATCC TGTGTCTCCC TTCCAGAACT   360
GAATGCTCAA GTCTTCTGTC ATAGTTCCAA CAATGTTACC AAAACCGAAT GCTGCTTCAC   420
AGATTTTTGC AACAACATAA CACTGCACCT TCCAACAGCA TCACCAAATG CCCCAAAACT   480
TGGACCCATG GAGCTGGCCA TCATTATTAC TGTGCCTGTT TGCCTCCTGT CCATAGCTGC   540
GATGCTGACA GTATGGGCAT GCCAGGGTCG ACAGTGCTCC TACAGGAAGA AAAAGAGACC   600
AAATGTGGAG GAACCACTCT CTGAGTGCAA TCTGGTAAAT GCTGGAAAAA CTCTGAAAGA   660
TCTGATTTAT GATGTGACCG CCTCTGGATC TGGCTCTGGT CTACCTCTGT TGGTTCAAAG   720
GACAATTGCA AGGACGATTG TGCTTCAGGA AATAGTAGGA AAAGGTAGAT TTGGTGAGGT   780
GTGGCATGGA AGATGGTGTG GGGAAGATGT GGCTGTGAAA ATATTCTCCT CCAGAGATGA   840
AAGATCTTGG TTTCGTGAGG CAGAAATTTA CCAGACGGTC ATGCTGCGAC ATGAAAACAT   900
CCTTGGTTTC ATTGCTGCTG ACAACAAAGA TAATGGAACT TGGACTCAAC TTTGGCTGGT   960
ATCTGAATAT CATGAACAGG GCTCCTTATA TGACTATTTG AATAGAAATA TAGTGACCGT  1020
GGCTGGAATG ATCAAGCTGG CGCTCTCAAT TGCTAGTGGT CTGGCACACC TTCATATGGA  1080
GATTGTTGGT ACACAAGGTA AACCTGCTAT TGCTCATCGA GACATAAAAT CAAAGAATAT  1140
CTTAGTGAAA AAGTGTGAAA CTTGTGCCAT AGCGGACTTA GGGTTGGCTG TGAAGCATGA  1200
TTCAATACTG AACACTATCG ACATACCTCA GAATCCTAAA GTGGGAACCA AGAGGTATAT  1260
GGCTCCTGAA ATGCTTGATG ATACAATGAA TGTGAATATC TTTGAGTCCT TCAAACGAGC  1320
TGACATCTAT TCTGTTGGTC TGGTTTACTG GGAAATAGCC CGGAGGTGTT CAGTCGGAGG  1380
AATTGTTGAG GAGTACCAAT TGCCTTATTA TGACATGGTG CCTTCAGATC CCTCGATAGA  1440
GGAAATGAGA AAGGTTGTTT GTGACCAGAA GTTTCGACCA AGTATCCCAA ACCAGTGGCA  1500
AAGTTGTGAA GCACTCCGAG TCATGGGGAG AATAATGCGT GAGTGTTGGT ATGCCAACGG  1560
AGCGGCCCGC CTAACTGCTC TTCGTATTAA GAAGACTATA TCTCAACTTT GTGTCAAAGA  1620
AGACTGCAAA GCCTAATGAT GATAATTATG TTAAAAAGAA ATCTCTCATA GCTTTCTTTT  1680
CCATTTTCCC CTTTATGTGA ATGTTTTTGC CATTTTTTTT TTGTTCTACC TCAAAGATAA  1740
GACAGTACAG TATTTAAGTG CCCATAAGGC AGCATGAAAA GATAACTCTA AAG          1793
```

(2)   INFORMATION FOR SEQ ID NO: 2:

    (i)   SEQUENCE CHARACTERISTICS:

        (A)   LENGTH: 493 amino acids
        (B)   TYPE: amino acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY: linear

    (ii)   MOLECULE TYPE: Peptide

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```
Met Thr Arg Ala Leu Cys Ser Ala Leu Arg Gln Ala Leu Leu Leu Leu
 1               5                  10                  15

Ala Ala Ala Ala Glu Leu Ser Pro Gly Leu Lys Cys Val Cys Leu Leu
            20                  25                  30
```

```
Cys Asp Ser Ser Asn Phe Thr Cys Gln Thr Glu Gly Ala Cys Trp Ala
    35                  40              45

Ser Val Met Leu Thr Asn Gly Lys Glu Gln Val Ile Lys Ser Cys Val
    50              55                  60

Ser Leu Pro Glu Leu Asn Ala Gln Val Phe Cys His Ser Ser Asn Asn
65              70              75                      80

Val Thr Lys Thr Glu Cys Cys Phe Thr Asp Phe Cys Asn Asn Ile Thr
                85              90                  95

Leu His Leu Pro Thr Ala Ser Pro Asn Ala Pro Lys Leu Gly Pro Met
            100             105                 110

Glu Leu Ala Ile Ile Ile Thr Val Pro Val Cys Leu Leu Ser Ile Ala
            115             120                 125

Ala Met Leu Thr Val Trp Ala Cys Gln Gly Arg Gln Cys Ser Tyr Arg
    130             135                 140

Lys Lys Lys Arg Pro Asn Val Glu Glu Pro Leu Ser Glu Cys Asn Leu
145             150             155                     160

Val Asn Ala Gly Lys Thr Leu Lys Asp Leu Ile Tyr Asp Val Thr Ala
                165             170                 175

Ser Gly Ser Gly Ser Gly Leu Pro Leu Leu Val Gln Arg Thr Ile Ala
            180             185                 190

Arg Thr Ile Val Leu Gln Glu Ile Val Gly Lys Gly Arg Phe Gly Glu
    195             200                 205

Val Trp His Gly Arg Trp Cys Gly Glu Asp Val Ala Val Lys Ile Phe
    210             215                 220

Ser Ser Arg Asp Glu Arg Ser Trp Phe Arg Glu Ala Glu Ile Tyr Gln
225             230             235                     240

Thr Val Met Leu Arg His Glu Asn Ile Leu Gly Phe Ile Ala Ala Asp
            245             250                 255

Asn Lys Asp Asn Gly Thr Trp Thr Gln Leu Trp Leu Val Ser Glu Tyr
            260             265                 270

His Glu Gln Gly Ser Leu Tyr Asp Tyr Leu Asn Arg Asn Ile Val Thr
    275             280                 285

Val Ala Gly Met Ile Lys Leu Ala Leu Ser Ile Ala Ser Gly Leu Ala
    290             295                 300

His Leu His Met Glu Ile Val Gly Thr Gln Gly Lys Pro Ala Ile Ala
305             310             315                     320

His Arg Asp Ile Lys Ser Lys Asn Ile Leu Val Lys Lys Cys Glu Thr
                325             330                 335

Cys Ala Ile Ala Asp Leu Gly Leu Ala Val Lys His Asp Ser Ile Leu
            340             345                 350

Asn Thr Ile Asp Ile Pro Gln Asn Pro Lys Val Gly Thr Lys Arg Tyr
    355             360                 365
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```
Met Ala Pro Glu Met Leu Asp Asp Thr Met Asn Val Asn Ile Phe Glu
    370             375                 380

Ser Phe Lys Arg Ala Asp Ile Tyr Ser Val Gly Leu Val Tyr Trp Glu
385             390                 395                     400

Ile Ala Arg Arg Cys Ser Val Gly Gly Ile Val Glu Glu Tyr Gln Leu
            405             410                 415

Pro Tyr Tyr Asp Met Val Pro Ser Asp Pro Ser Ile Glu Glu Met Arg
            420             425                 430

Lys Val Val Cys Asp Gln Lys Phe Arg Pro Ser Ile Pro Asn Gln Trp
        435             440                 445

Gln Ser Cys Glu Ala Leu Arg Val Met Gly Arg Ile Met Arg Glu Cys
    450             455                 460

Trp Tyr Ala Asn Gly Ala Ala Arg Leu Thr Ala Leu Arg Ile Lys Lys
465             470             475                     480

Thr Ile Ser Gln Leu Cys Val Lys Glu Asp Cys Lys Ala
                485                 490
```

(2)   INFORMATION FOR SEQ ID NO: 3:

    (i)   SEQUENCE CHARACTERISTICS:

        (A)   LENGTH: 8 amino acids
        (B)   TYPE: amino acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY: linear

    (ii) MOLECULE TYPE: Peptide

    (ix) FEATURE:

        (D)   OTHER INFORMATION: "Xaa" in positions 6 and 7 stand
                              for an unspecified amino acid.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

```
His Arg Asp Leu Lys Xaa Xaa Asn
 1               5
```

(2)   INFORMATION FOR SEQ ID NO: 4:

    (i)   SEQUENCE CHARACTERISTICS:

        (A)   LENGTH: 23 base pairs
        (B)   TYPE: nucleic acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY: linear

    (ix) FEATURE:

        (D)   OTHER INFORMATION: The letter "R" stands for A or G.
                              The letter "N" stands for Inosine.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

GARRARGTNG CNGTNAARRT NTT   23

(2) INFORMATION FOR SEQ ID NO: 5:

    (i) SEQUENCE CHARACTERISTICS:

          (A) LENGTH: 29 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

    (ix) FEATURE:

          (D) OTHER INFORMATION: The letter "R" stands for A or G.
                                    The letter "N" stands for Inosine.
                                    The letter "K" stands for G or T.
                                    The letter "M" stands for A or C.
                                    The letter "Y" stands for C or T.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

TTRATRTCNC KRTGNGMNAT NGMNGGYTT   29

(2) INFORMATION FOR SEQ ID NO: 6:

    (i) SEQUENCE CHARACTERISTICS:

          (A) LENGTH: 8 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: Peptide

    (ix) FEATURE:

          (D) OTHER INFORMATION: "Xaa" in position 2 stands for Lys or
                                     Glu. "Xaa" in position 7 stands for
                                     Val or Ile.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Glu Xaa Val Ala Val Lys Xaa Phe
 1   5

(2) INFORMATION FOR SEQ ID NO: 7:

    (i) SEQUENCE CHARACTERISTICS:

          (A) LENGTH: 10 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: Peptide

(ix) FEATURE:

            (D)   OTHER INFORMATION: "Xaa" in position 3 stands for Ala or
                                         Ser. "Xaa" in position 5 stands for
                                         Ala or Ser.

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Lys Pro Xaa Ile Xaa His Arg Asp Ile Lys
 1   5   10

(2)   INFORMATION FOR SEQ ID NO: 8:

      (i)   SEQUENCE CHARACTERISTICS:

            (A)   LENGTH: 24 base pairs
            (B)   TYPE: nucleic acid
            (C)   STRANDEDNESS: single
            (D)   TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

AACTTTGGCT GGTATCTGAA TATC   24

(2)   INFORMATION FOR SEQ ID NO: 9:

      (i)   SEQUENCE CHARACTERISTICS:

            (A)   LENGTH: 24 base pairs
            (B)   TYPE: nucleic acid
            (C)   STRANDEDNESS: single
            (D)   TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

CCTTGTGTAC CAACAATCTC CATA   24

(2)   INFORMATION FOR SEQ ID NO: 10:

      (i)   SEQUENCE CHARACTERISTICS:

            (A)   LENGTH: 22 base pairs
            (B)   TYPE: nucleic acid
            (C)   STRANDEDNESS: single
            (D)   TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

CTCCAGAGAT GAGAGATCTT GG   .   22

(2)   INFORMATION FOR SEQ ID NO: 11:

      (i)   SEQUENCE CHARACTERISTICS:

            (A)   LENGTH: 22 base pairs
            (B)   TYPE: nucleic acid
            (C)   STRANDEDNESS: single
            (D)   TOPOLOGY: linear

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TTCCAGCCAC GGTCACTATG TT   22

(2)   INFORMATION FOR SEQ ID NO: 12:

    (i)   SEQUENCE CHARACTERISTICS:

        (A)   LENGTH: 13 amino acids
        (B)   TYPE: amino acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY: linear

    (ii) MOLECULE TYPE: Peptide

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Tyr Arg Lys Lys Lys Arg Pro Asn Val Glu Glu Pro Leu
1   5   10

(2)   INFORMATION FOR SEQ ID NO: 13:

    (i)   SEQUENCE CHARACTERISTICS:

        (A)   LENGTH: 10 amino acids
        (B)   TYPE: amino acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY: linear

    (ii) MOLECULE TYPE: Peptide

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser
1   5   10

(2)   INFORMATION FOR SEQ ID NO: 14:

    (i)   SEQUENCE CHARACTERISTICS:

        (A)   LENGTH: 48 base pairs
        (B)   TYPE: nucleic acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

CTTCGAAAGC TTGAAATCGG TACCATCGAT TCTAGAGTTA ACTTCGAA   48

(2)   INFORMATION FOR SEQ ID NO: 15:

    (i)   SEQUENCE CHARACTERISTICS:

        (A)   LENGTH: 47 base pairs
        (B)   TYPE: nucleic acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY: linear

CTCTAGAACG CGTTAAGGCG CGCCAATATC GATGAATTCT TCGAAGC   47